#7

1646

# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Ling, et al

Serial No: 09/883,848

Filed: June 18, 2001

For: Angiogenesis-Modulating Compositions and Uses

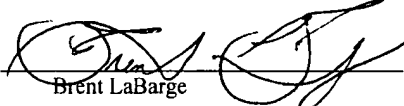Attorney Docket No. CIBT-P01-119

Art Unit: 1646

Examiner: Not Assigned

**COPY OF PAPERS ORIGINALLY FILED**

*(stamp: OIPE MAIL DATE CANCELLED PATENT & TRADEMARK OFFICE)*

*(stamp: MAR 0 6 2002)*

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*(stamp: RECEIVED MAR 1 3 2002 TECH CENTER 1600/2900)*

## TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING IN COMPUTER READABLE FORM

## IN COMPLIANCE WITH 37 C.F.R. §1.825

Box Sequence
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This amendment is submitted in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures mailed on February 15, 2002; a copy is attached.

Transmitted herewith is a copy of a "Substitute Sequence Listing" in paper form for the above-identified patent application as required by 37 C.F.R. §1.825(a), and a copy of the "Substitute Sequence Listing" in computer readable form as required by 37 C.F.R. §§ 1.825(b).

As required by 37 C.F.R. § 1.825(b), Applicant's Agent hereby states that the contents of the Substitute "Sequence Listing" in paper form and in the computer readable form submitted herewith are the same and, as required by 37 C.F.R. § 1.825(a), also states that the submission includes no new matter.

Respectfully Submitted,

Date: February 26, 2002

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Registration No.: 44,735

*Customer No: 28120*
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Boston, MA 02110
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COPY

MAIL DATE CANCELLED COPY

UNITED STATES PATENT AND TRADEMARK OFFICE

| APPLICATION NUMBER | FILING/RECEIPT DATE | FIRST NAMED APPLICANT | ATTORNEY DOCKET NUMBER |
|---|---|---|---|
| 09/883,848 | 06/18/2001 | Leona E. Ling | CIBT-P01-119 |

28120
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BOSTON, MA 02110-2624

Ropes & Gray
Intellectual Property Dept.

FEB 2 0 2002

**CONFIRMATION NO. 9957**
**FORMALITIES LETTER**

*OC000000007482459*

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Date Mailed: 02/15/2002

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MAR 1 3 2002

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase PatentIn Software, call (703) 306-2600**
- **For PatentIn Software Program Help, call (703) 306-4119 or e-mail at**
- **patin21help@uspto.gov or patin3help@uspto.gov**

*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center
Initial Patent Examination Division (703) 308-1202
PART 1 - ATTORNEY/APPLICANT COPY

R&G Docket No.: CIBT-P01-119
Action: SEQ Listing
Stat. Deadline: 15Apr02

OIPE
MAIL DATE CANCELLED

OIPE
MAR 0 6 2002

UNITED STATES PATENT AND TRADEMARK OFFICE
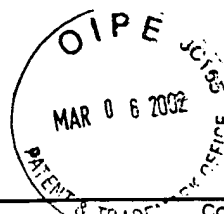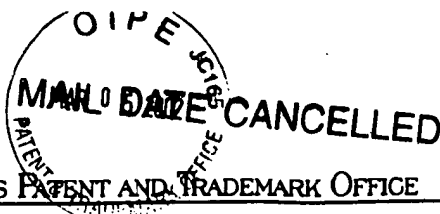
COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

| APPLICATION NUMBER | FILING/RECEIPT DATE | FIRST NAMED APPLICANT | ATTORNEY DOCKET NUMBER |
|---|---|---|---|
| 09/883,848 | 06/18/2001 | Leona E. Ling | CIBT-P01-119 |

**CONFIRMATION NO. 9957**

28120
ROPES & GRAY
ONE INTERNATIONAL PLACE
BOSTON, MA 02110-2624

COPY OF PAPERS
ORIGINALLY FILED

**FORMALITIES LETTER**
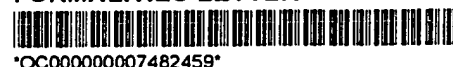
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RECEIVED

MAR 1 5 2002

TECH CENTER 1600-2900

Date Mailed: 02/15/2002

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

**For questions regarding compliance to these requirements, please contact:**

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase Patentin Software, call (703) 306-2600**
- **For Patentin Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov**

*A copy of this notice __MUST__ be returned with the reply.*

Customer Service Center
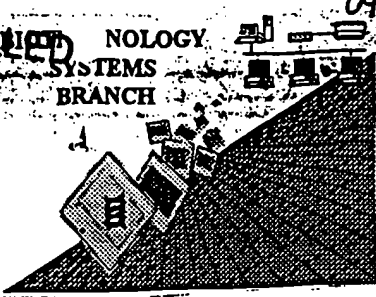Initial Patent Examination Division (703) 308-1202
PART 2 - COPY TO BE RETURNED WITH RESPONSE

# RAW SEQUENCE LISTING
## ERROR REPORT

MAR 0 6 2002

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/883,848

Source: OIPE

Date Processed by STIC: 10/12/2001

RECEIVED MAR 1 3 2002 TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _09/883,848_ |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAF**

1 ____ Wrapped Nucleics  Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

· 3 ____ Misaligned Amino  Numbering
The numbering under each $5^{th}$ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0  "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences  (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences  (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's  (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>  Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0  "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001
TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt
Output Set: N:\CRF3\10122001\I883848.raw

Does Not Comply
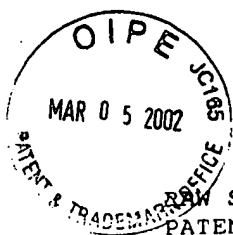Corrected Diskette Needed

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 3 <110> APPLICANT: Ling, L.
 4        Sanicola-Nadel, M.
 6 <120> TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
 8 <130> FILE REFERENCE: CIBT-P01-119
10 <140> CURRENT APPLICATION NUMBER: 09/883,848
11 <141> CURRENT FILING DATE: 2001-09-24
13 <150> PRIOR APPLICATION NUMBER: 60/211,919
14 <151> PRIOR FILING DATE: 2000-06-16
16 <160> NUMBER OF SEQ ID NOS: 48
18 <170> SOFTWARE: PatentIn Ver. 2.1
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**ERRORED SEQUENCES**

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167 <210> SEQ ID NO: 6
168 <211> LENGTH: 1425
169 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 6
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174 ggactggcgt gcggaccggg cagggggttc gggaagagga ggcaccccaa aaagctgacc 120
175 cctttagcct acaagcagtt tatccccaat gtggccgaga agaccctagg cgccagcgga 180
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185 ttcctggacc gcgacgacgg cgccaagaag gtcttctacg tgatcgagac gcgggagccg 780
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188 cctcgggcgc tgttcgccag ccgcgtgcgc ccgggccagc gcgtgtacgt ggtggccgag 960
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190 gccgcgggcg cctacgcgcc gctcacggca agctgggcgc accgggcctt cgcgcccttc 1140
191 gcctcgtgct acgcggtcat cgaggagcac agctgggcgc accgggcctt cgcgcccttc 1140
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193 agcggcggcg gggaccgcgg gggcggcggc ggcagagtag ccctaaccgc tccaggtgct 1260
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195 caaataggca cctggctcct ggacagcgag gccctgcacc cgctgggcat ggcggtcaag 1380
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196 tccagcnnna gccgggggggc cggggggaggg gcgcgggagg gggcc
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E→ 196 tccagc~~nnn~~a gccgggggggc cggggggaggg gcgcgggagg gggcc → see item 9 on Error Summary Sheet

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728 <210> SEQ ID NO: 15
729 <211> LENGTH: 475
730 <212> TYPE: PRT
731 <213> ORGANISM: Homo sapiens
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P.3

10/12/01

SEQUENCE LISTING
PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001
TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt
Output Set: N:\CRF3\10122001\I883848.raw

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735  1               5                  10                 15
737 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
738          20                 25                 30
740 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
741          35                 40                 45
743 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
744          50                 55                 60
746 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
747  65                 70                 75                 80
749 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
750                  85                 90                 95
752 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
753          100                105                110
755 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
756          115                120                125
758 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
759          130                135                140
761 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
762 145                150                155                160
764 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
765          165                170                175
767 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
768          180                185                190
770 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
771          195                200                205
773 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
774          210                215                220
776 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
777 225                230                235                240
779 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
780                  245                250                255
782 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
783          260                265                270
785 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
786          275                280                285
788 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
789          290                295                300
791 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
792 305                310                315                320
794 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
795          325                330                335
797 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
798          340                345                350
800 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
801          355                360                365
803 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
804          370                375                380
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001
TIME: 12:14:38

Input Set : A:\CIBT-P01-119 Seq List.txt
Output Set: N:\CRF3\10122001\I883848.raw

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    807 385                 390             395             400
    809 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
    810             405             410                 415
    812 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
    813             420             425                 430
    815 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
    816         435             440             445
E--> 818 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
    819     450             455             460
    821 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
    822 465             470             475
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   1349 <211> LENGTH: (174) 175 shown
   1350 <212> TYPE: PRT
   1351 <213> ORGANISM: Homo sapiens
   1353 <400> SEQUENCE: 23
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   1358             20              25              30
   1360 Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser
   1361         35              40              45
   1363 Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe
   1364     50              55              60
   1366 Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys
   1367  65              70              75              80
   1369 Lys Asp Arg Leu Asn Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro
   1370             85              90              95
   1372 Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His
   1373         100             105             110
   1375 Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr
   1376         115             120             125
   1378 Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val
   1379     130             135             140
   1381 Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His
   1382 145             150             155             160
   1384 Cys Ser Val Lys Ser Glu His Ser Ala Ala Ala Lys Thr Gly Gly
E--> 1385             165             170                 175
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

10/12/01

Sl    "C\CRF3\Outhold\VcrI883848.htm

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/883,848

DATE: 10/12/2001
TIME: 12:14:39

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Output Set: N:\CRF3\10122001\I883848.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:196 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:818 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:1385 M:252 E: No. of Seq. differs, <211>LENGTH:Input:174 Found:175 SEQ:23
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
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L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

SEQUENCE LISTING

<110> Ling, L.
      Sanicola-Nadel, M.

<120> ANGIOGENESIS-MODULATING COMPOSITIONS AND USES

<130> CIBT-P01-119

<140> 09/883,848
<141> 2001-06-18

<150> 60/211,919
<151> 2000-06-16

<160> 48

<170> PatentIn Ver. 2.1

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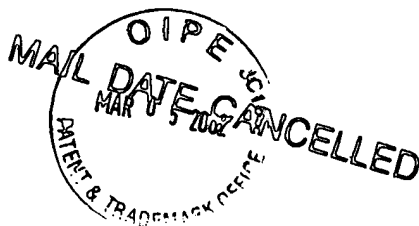gtggcaccgg ccagctg 1277

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<212> DNA
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<212> DNA
<213> Brachydanio rerio

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<213> Gallus gallus

<400> 10

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Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
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Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
     50                  55                  60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65                  70                  75                  80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
                 85                  90                  95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
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Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
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Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
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Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
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Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
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Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
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Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
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His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
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Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
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Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
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His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
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Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
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Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
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Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
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Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
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Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
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Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
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Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
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<213> Mus musculus

<400> 11
Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
  1             5             10                  15

Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
            20              25                  30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
        35              40              45

Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu

50                       55                          60

      Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
      65                       70                    75                    80

      Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
                          85                    90                    95

      Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
                      100                   105                   110

      Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
                  115                   120                   125

      Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
              130                   135                   140

      Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
      145                   150                   155                   160

      Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
                      165                   170                   175

      Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
                  180                   185                   190

      Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
                  195                   200                   205

      Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
          210                   215                   220

      Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
      225                   230                   235                   240

      Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
                      245                   250                   255

      Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
                  260                   265                   270

      Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
                  275                   280                   285

      Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
          290                   295                   300

      Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
      305                   310                   315                   320

      Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
                      325                   330                   335

      Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
                  340                   345                   350

      Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala

```
          355                     360                     365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
    370                 375                 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385                 390                 395


<210> 12
<211> 411
<212> PRT
<213> Mus musculus

<400> 12
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
  1               5                  10                  15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
            20                  25                  30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
        35                  40                  45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
    50                  55                  60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65                  70                  75                  80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
                85                  90                  95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
            100                 105                 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
        115                 120                 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
    130                 135                 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145                 150                 155                 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
            165                 170                 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
            180                 185                 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
        195                 200                 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
    210                 215                 220
```

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225                 230             235                 240


Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
                245             250             255


Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
            260             265             270


Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
        275             280             285


His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
    290             295             300


Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305             310             315                 320


Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
            325             330             335


Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
            340             345             350


Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
        355             360             365


Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
    370             375             380


Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
385             390             395                 400


Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
                405             410


<210> 13
<211> 437
<212> PRT
<213> Mus musculus

<400> 13
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1           5               10              15


Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
            20              25              30


Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
        35              40              45


Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
    50              55              60


Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn

```
         65                    70                    75                    80
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
                85                    90                    95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
                100                   105                   110

Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
            115                   120                   125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
        130                   135                   140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
145                   150                   155                   160

Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
                165                   170                   175

Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
            180                   185                   190

Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
            195                   200                   205

Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
    210                   215                   220

Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
225                   230                   235                   240

Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
                245                   250                   255

Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
            260                   265                   270

Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
            275                   280                   285

Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
    290                   295                   300

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
305                   310                   315                   320

Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
                325                   330                   335

His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
            340                   345                   350

Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
        355                   360                   365

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
```

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385                     390                 395                     400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
                    405                 410                 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
                420                 425                 430

Ala Val Lys Ser Ser
            435


<210> 14
<211> 418
<212> PRT
<213> Brachydanio rerio

<400> 14
Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
    1                   5                   10                  15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
                20                  25                  30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
            35                  40                  45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
        50                  55                  60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65                  70                  75                  80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
                85                  90                  95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
            100                 105                 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
        115                 120                 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
        130                 135                 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145                 150                 155                 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
                165                 170                 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
                180                 185                 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
        195                 200                 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
        210                 215                 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
225                 230                 235                 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
                245                 250                 255

Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
            260                 265                 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
        275                 280                 285

Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
        290                 295                 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
305                 310                 315                 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
                325                 330                 335

Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
            340                 345                 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
        355                 360                 365

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
        370                 375                 380

Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385                 390                 395                 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
                405                 410                 415

Ser Ser


<210> 15
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (463)
<223> Xaa=unknown amino acid residue

<400> 15

```
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1               5                  10                  15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
             20              25                  30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
         35                  40                  45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
     50                  55                  60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65                  70                  75                  80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
             85                  90                  95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
         100                 105                 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
         115                 120                 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
     130                 135                 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
145                 150                 155                 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
             165                 170                 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
         180                 185                 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
         195                 200                 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
     210                 215                 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
225                 230                 235                 240

Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
             245                 250                 255

Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
         260                 265                 270

Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
         275                 280                 285

Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
     290                 295                 300
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```
Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
305                 310             315                 320

Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
                325             330             335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
            340             345             350

Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
        355             360             365

Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
    370             375             380

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
385             390             395             400

Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr
            405             410             415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
        420             425             430

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
        435             440             445

Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
    450             455             460

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465             470             475


<210> 16
<211> 411
<212> PRT
<213> Homo sapiens

<400> 16
Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1           5               10              15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
            20              25              30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
        35              40              45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
    50              55              60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65              70              75              80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
            85              90              95
```

```
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
        100                 105                 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
        115                 120                 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
    130                 135                 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145                 150                 155                 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
            165                 170                 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
            180                 185                 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
        195                 200                 205

Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
    210                 215                 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
225                 230                 235                 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
            245                 250                 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
            260                 265                 270

Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
        275                 280                 285

Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
    290                 295                 300

Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305                 310                 315                 320

Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
            325                 330                 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
            340                 345                 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
        355                 360                 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
    370                 375                 380

Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser
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                385                      390                      395                      400
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
                    405                      410


<210> 17
<211> 396
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1               5                  10                      15

Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
                20                  25                      30

Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
            35                  40                  45

Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
        50                  55                  60

Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65                  70                  75                      80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
                85                  90                      95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
            100                 105                 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
        115                 120                 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
    130                 135                 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145                 150                 155                 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
                165                 170                 175

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
            180                 185                 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
            195                 200                 205

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
    210                 215                 220

Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
```

```
                    225                     230                     235                     240
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
                245                 250                 255

Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
            260             265             270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
        275             280             285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
        290             295             300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305             310             315             320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
            325             330             335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
            340             345             350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
        355             360             365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
    370             375             380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385             390             395


<210> 18
<211> 416
<212> PRT
<213> Brachydanio rerio

<400> 18
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
  1           5               10                  15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
            20              25              30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
        35              40              45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
    50              55              60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65              70              75              80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
            85              90              95
```

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
            100                 105                 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
            115                 120                 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
            130                 135                 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145                 150                 155                 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
                165                 170                 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
            180                 185                 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
            195                 200                 205

Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
    210                 215                 220

Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
225                 230                 235                 240

Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
                245                 250                 255

Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
            260                 265                 270

His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
            275                 280                 285

Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
    290                 295                 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
305                 310                 315                 320

Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
                325                 330                 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
                340                 345                 350

Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
            355                 360                 365

Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
    370                 375                 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
385                 390                 395                 400

```
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
             405                 410                 415




<210> 19
<211> 1416
<212> DNA
<213> Drosophila melanogaster

<220>
<221> CDS
<222> (1)..(1413)

<400> 19
atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc      48
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
  1               5                  10                  15

tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag      96
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
             20                  25                  30

ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg     144
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
             35                  40                  45

caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg     192
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
         50                  55                  60

acc tct ctg gtg gcc ctg ctg ctg atc gtc ttg ccg atg gtc ttt agc     240
Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65                  70                  75                  80

ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg     288
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
                 85                  90                  95

cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc     336
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
             100                 105                 110

gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg     384
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
             115                 120                 125

gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc     432
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
         130                 135                 140

ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag     480
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
145                 150                 155                 160
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cgc tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa    528
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
            165                 170                 175

tgg ccc ggc atc cgg ctg ctg gtc acc gag agc tgg gac gag gac tac    576
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
            180                 185                 190

cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att    624
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
            195                 200                 205

gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg    672
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
        210                 215                 220

gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac    720
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
225                 230                 235                 240

atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac    768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
            245                 250                 255

ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg    816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
            260                 265                 270

aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc    864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
            275                 280                 285

gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc    912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
        290                 295                 300

aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga    960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
305                 310                 315                 320

gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg    1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
            325                 330                 335

gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag    1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
            340                 345                 350

aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag    1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
            355                 360                 365

cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg    1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
            370                 375                 380
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ctg acc cgc gag ggc acc att gtg gtc aac tcg gtg gcc gcc agt tgc      1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385                 390                 395                 400

tat gcg gtg atc aac agt cag tcg ctg gcc cac tgg gga ctg gct ccc      1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
                    405                 410                 415

atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag      1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
                420                 425                 430

ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc      1344
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
                435                 440                 445

atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg      1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
                450                 455                 460

ccg cag agc tgg cgc cac gat tga                                      1416
Pro Gln Ser Trp Arg His Asp
465                 470


<210> 20
<211> 471
<212> PRT
<213> Drosophila melanogaster

<400> 20
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
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Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
                20                  25                  30

Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
                35                  40                  45

Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
        50                  55                  60

Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65                  70                  75                  80

Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
                85                  90                  95

Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
                100                 105                 110

Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
        115                 120                 125

Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
        130                 135                 140
```

Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
145                150                155                160

Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
                165                170                175

Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
                180                185                190

His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
                195                200                205

Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
        210                215                220

Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
225                230                235                240

Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
                245                250                255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
                260                265                270

Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
        275                280                285

Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
        290                295                300

Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
305                310                315                320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
                325                330                335

Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
        340                345                350

Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
        355                360                365

Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
        370                375                380

Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385                390                395                400

Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
                405                410                415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
                420                425                430

Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly

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Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
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Pro Gln Ser Trp Arg His Asp
465                    470
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<210> 21
<211> 522
<212> DNA
<213> Homo sapiens

<400> 21
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gggaagatct ccagaaactc cgagcgattt aaggaactca cccccaatta caaccccgac 180
atcatattta aggatgaaga aaacaccgga gcggacaggc tgatgactca gaggtgtaag 240
gacaagttga acgctttggc catctcggtg atgaaccagt ggccaggagt gaaactgcgg 300
gtgaccgagg ctgggacga agatggccac cactcagagg agtctctgca ctacgagggc 360
cgcgcagtgg acatcaccac gtctgaccgc gaccgcagca agtacggcat gctggcccgc 420
ctggcggtgg aggccggctt cgactgggtg tactacgagt ccaaggcaca tatccactgc 480
tcggtgaaag cagagaactc ggtggcggcc aaatcgggag gc            522
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<210> 22
<211> 525
<212> DNA
<213> Homo sapiens

<400> 22
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gaaggcaaga tcgctcgcag ctccgagcgc ttcaaggagc tcacccccaa ttacaatcca 180
gacatcatct tcaaggacga ggagaacaca ggcgccgacc gcctcatgac ccagcgctgc 240
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cgcttggcag tggaggccgg cttttgactgg gtgtattacg agtcaaaggc ccacgtgcat 480
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<210> 23
<211> 175
<212> PRT
<213> Homo sapiens

<400> 23
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Cys Gly Pro Gly Arg Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys
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Leu Val Pro Leu Ala Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys
            20                  25                  30

Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser
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Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe
    50                  55                  60

Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys
65                  70                  75                  80

Lys Asp Arg Leu Asn Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro
            85                  90                  95

Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His
            100                 105                 110

Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr
        115                 120                 125

Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val
    130                 135                 140

Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His
145                 150                 155                 160

Cys Ser Val Lys Ser Glu His Ser Ala Ala Ala Lys Thr Gly Gly
                165                 170                 175


<210> 24
<211> 174
<212> PRT
<213> Homo sapiens

<400> 24
Cys Gly Pro Gly Arg Gly Phe Gly Lys Arg Arg His Pro Lys Lys Leu
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Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
            20                  25                  30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ser Arg Asn Ser Glu
            35                  40                  45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
    50                  55                  60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65                  70                  75                  80

Asp Lys Leu Asn Ala Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly
            85                  90                  95

Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser
            100                 105                 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
        115                 120                 125
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Asp Arg Asp Arg Ser Lys Tyr Gly Met Leu Ala Arg Leu Ala Val Glu
    130                 135             140

Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145                 150             155                 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly
                165             170


<210> 25
<211> 176
<212> PRT
<213> Homo sapiens

<400> 25
Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys
  1             5                 10                  15

Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu
                20              25                  30

Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly
            35              40                  45

Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile
      50              55                  60

Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg
 65              70                  75                  80

Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp
            85                  90                  95

Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His
            100             105                 110

His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr
        115             120                 125

Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala
    130             135                 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Val
145             150                 155                 160

His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly
                165             170                 175



<210> 26
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

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<223> Xaa=Cys that may be modified, altered or
      substituted within another moiety or series of
      moieties as described herein

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<222> (6)
<223> Xaa=Val or Gly

<220>
<221> SITE
<222> (7)
<223> Xaa=Val, Glu or Pro

<220>
<221> SITE
<222> (8)
<223> Xaa=Gly or Val

<220>
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<222> (9)
<223> Xaa=Ser or Gly

<220>
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<222> (10)
<223> Xaa=Arg or Lys

<220>
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<222> (13)
<223> Xaa=Pro, His or Tyr

<220>
<221> SITE
<222> (14)
<223> Xaa=Pro or Ala

<220>
<221> SITE
<222> (15)
<223> Xaa=Arg or Lys

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<222> (17)
<223> Xaa=any amino acid

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<223> Xaa=Val or Thr

<220>
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<222> (22)
<223> Xaa=Ala or Leu

<220>
<221> SITE
<222> (27)
<223> Xaa=Ser, Ile or Val

<220>
<221> SITE
<222> (29)
<223> Xaa=Asn or Gly

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<222> (31)
<223> Xaa=Pro ar Ala

<220>
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<222> (41)
<223> Xaa=Tyr or Ala

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<223> Xaa=Ile or Val

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<223> Xaa=Ser, Asn or Gly

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<223> Xaa=Glu or Asp

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<223> Xaa=Thr or Val

<220>
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<222> (71)
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<223> Xaa=Asp or Glu

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<222> (84)
<223> Xaa=Arg or Lys

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<222> (85)
<223> Xaa=Leu or Val

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<223> Xaa=Ser or Ala

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<223> Xaa=Gln or Met

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<223> Xaa=Glu or Asp

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<220>
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<223> Xaa=Ala or Asn

<220>
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<222> (160)
<223> Xaa=Val or Ile

<220>
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<223> Xaa=Cys or Val

<220>
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<220>
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<223> Xaa=Ala, Val or Leu

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<223> Xaa=Lys or Arg

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<223> Xaa=Thr, Ser or Ala

<400> 26
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Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Val Xaa Glu
            20                  25                  30
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Lys Thr Leu Gly Ala Ser Gly Arg Xaa Glu Gly Lys Xaa Xaa Arg Xaa
         35                  40                  45

Ser Glu Arg Phe Lys Xaa Leu Xaa Pro Asn Tyr Asn Pro Asp Ile Ile
     50                  55                  60


Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65                  70                  75                  80

Cys Lys Xaa Xaa Xaa Asn Ser Leu Ala Ile Xaa Val Met Asn Xaa Trp
             85                  90                  95

Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His
         100                 105                 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr
         115                 120                 125

Thr Ser Asp Arg Asp Arg Xaa Lys Tyr Gly Xaa Leu Ala Arg Leu Ala
     130                 135                 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
145                 150                 155                 160

His Xaa Ser Val Lys Xaa Xaa Xaa Xaa Ala Ala Xaa Xaa Gly Gly
             165                 170                 175


<210> 27
<211> 528
<212> DNA
<213> Homo sapiens

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gcggagggga gggtggcaag gggctccgag cgcttccggg acctcgtgcc caactacaac 180
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gcgcgcctcg cagtggaagc cggcttcgac tgggtctact acgagtcccg caaccacgtc 480
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<210> 28
<211> 684
<212> DNA
<213> Homo sapiens

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acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 180
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta ccagagcacg 240
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<210> 29
<211> 687
<212> DNA
<213> Homo sapiens

<400> 29
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<210> 30
<211> 702
<212> DNA
<213> Homo sapiens

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aatcaccaca cgactaagag cttctcccgg actccgggta aa 702


<210> 31
<211> 9776
<212> DNA
<213> Plasmid P55

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